



Figure 1A: Nucleotide and amino acid sequences (SEQ ID Nos: 1 and 2) of the ATP/ADP translocase from Chlamydia pneumoniae

gaaataaaaa actatcagaa tagaaaataa aagtattttca gagggtaa atg aca		56
Met Thr		
1		
aaa acc gaa gaa aaa cct ttt gga aaa ttg cgc tct ttc ttg tgg ccg		104
Lys Thr Glu Glu Lys Pro Phe Gly Lys Leu Arg Ser Phe Leu Trp Pro		
5 10 15		
ata cat act cac gag cta aag aaa gtt ctg cca atg ttc cta atg ttc		152
Ile His Thr His Glu Leu Lys Lys Val Leu Pro Met Phe Leu Met Phe		
20 25 30		
ttc tgt att aca ttt aac tat acg gtg tta cgc gat aca aaa gac act		200
Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys Asp Thr		
35 40 45 50		
ctt att gtg gga gct cct ggt tct ggt gca gag gca ata cct ttc atc		248
Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro Phe Ile		
55 60 65		
aag ttt tgg ctt gtt gtc ccc tgt gct att atc ttt atg ctt att tat		296
Lys Phe Trp Leu Val Val Pro Cys Ala Ile Ile Phe Met Leu Ile Tyr		
70 75 80		
gca aag cta agt aat att tta agt aag cag gcc tta ttt tat gca gtg		344
Ala Lys Leu Ser Asn Ile Leu Ser Lys Gln Ala Leu Phe Tyr Ala Val		
85 90 95		
gga acg ccc ttt tta att ttc ttt gcc ctg ttc ccg act gta att tat		392
Gly Thr Pro Phe Leu Ile Phe Phe Ala Leu Phe Pro Thr Val Ile Tyr		
100 105 110		
ccg cta cgc gat gtt tta cat cct aca gaa ttt gct gac cgt tta cag		440
Pro Leu Arg Asp Val Leu His Pro Thr Glu Phe Ala Asp Arg Leu Gln		
115 120 125 130		
gcc atc cta cct cca gga ttg cta gga ctc gtt gcc atc tta aga aac		488
Ala Ile Leu Pro Pro Gly Leu Leu Gly Leu Val Ala Ile Leu Arg Asn		
135 140 145		
tgg aca ttt gct gca ttt tat gta ctt gct gaa cta tgg gga agc gtc		536
Trp Thr Phe Ala Ala Phe Tyr Val Leu Ala Glu Leu Trp Gly Ser Val		
150 155 160		
atg cta tct cta atg ttc tgg gga ttt gct aat gaa att aca aaa atc		584
Met Leu Ser Leu Met Phe Trp Gly Phe Ala Asn Glu Ile Thr Lys Ile		
165 170 175		
cac gaa gca aag cgt ttc tac gct ctt ttc ggt atc gga gct aat att		632
His Glu Ala Lys Arg Phe Tyr Ala Leu Phe Gly Ile Gly Ala Asn Ile		
180 185 190		



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Appl. No.: 09/869,433

Figure 1B (Continuation of Figure 1)

tct tta cta gct tct ggt cgt gca att gtt tgg gct tca aag ttg aga	680
Ser Leu Leu Ala Ser Gly Arg Ala Ile Val Trp Ala Ser Lys Leu Arg	
195 200 205 210	
gct tcc gtt tct gaa ggt gta gat cct tgg gga att tct tta cgt ctt	728
Ala Ser Val Ser Glu Gly Val Asp Pro Trp Gly Ile Ser Leu Arg Leu	
215 220 225	
ttg atg gct atg act att gta tct gga ctt gtt ctt atg gcc agt tac	776
Leu Met Ala Met Thr Ile Val Ser Gly Leu Val Leu Met Ala Ser Tyr	
230 235 240	
tgg tgg atc aat aag aac gta ttg acc gat cct cgc ttc tat aat cca	824
Trp Trp Ile Asn Lys Asn Val Leu Thr Asp Pro Arg Phe Tyr Asn Pro	
245 250 255	
gaa gaa atg caa aag ggg aaa aaa ggt gct aaa cct aaa atg aat atg	872
Glu Glu Met Gln Lys Gly Lys Lys Gly Ala Lys Pro Lys Met Asn Met	
260 265 270	
aaa gat agc ttc ctc tat ctt gat aga tct cct tat att ctt tta tta	920
Lys Asp Ser Phe Leu Tyr Leu Asp Arg Ser Pro Tyr Ile Leu Leu Leu	
275 280 285 290	
act ctc ttg gtt att gcc tat ggt att tgc att aac tta atc gaa gtg	968
Thr Leu Leu Val Ile Ala Tyr Gly Ile Cys Ile Asn Leu Ile Glu Val	
295 300 305	
act tgg aaa agt cag ctg aaa ctg caa tat cct aat atg aat gac tat	1016
Thr Trp Lys Ser Gln Leu Lys Leu Gln Tyr Pro Asn Met Asn Asp Tyr	
310 315 320	
agt gag ttc atg ggg aac ttc tcc ttc tgg act ggc gta gta tcc gta	1064
Ser Glu Phe Met Gly Asn Phe Ser Phe Trp Thr Gly Val Val Ser Val	
325 330 335	
ctt atc atg cta ttt gtt ggt ggt aac gtc att cgt aaa ttt gga tgg	1112
Leu Ile Met Leu Phe Val Gly Gly Asn Val Ile Arg Lys Phe Gly Trp	
340 345 350	
tta act gga gcc cta gtc act cct gtc atg gtt ctc cta aca ggt atc	1160
Leu Thr Gly Ala Leu Val Thr Pro Val Met Val Leu Leu Thr Gly Ile	
355 360 365 370	
gtt ttc ttc gct ctt gtt atc ttt aga aac caa gct tct ggg ctg gtc	1208
Val Phe Phe Ala Leu Val Ile Phe Arg Asn Gln Ala Ser Gly Leu Val	
375 380 385	
gct atg ttc ggt aca act cct ctc atg cta gct gtg gtt gtc gga gct	1256
Ala Met Phe Gly Thr Thr Pro Leu Met Leu Ala Val Val Val Gly Ala	
390 395 400	
ata cag aat att ctt tcg aaa tcc aca aaa tac gct ctc ttt gac tca	1304
Ile Gln Asn Ile Leu Ser Lys Ser Thr Lys Tyr Ala Leu Phe Asp Ser	
405 410 415	



Figure 1C (Continuation of Figure 1)

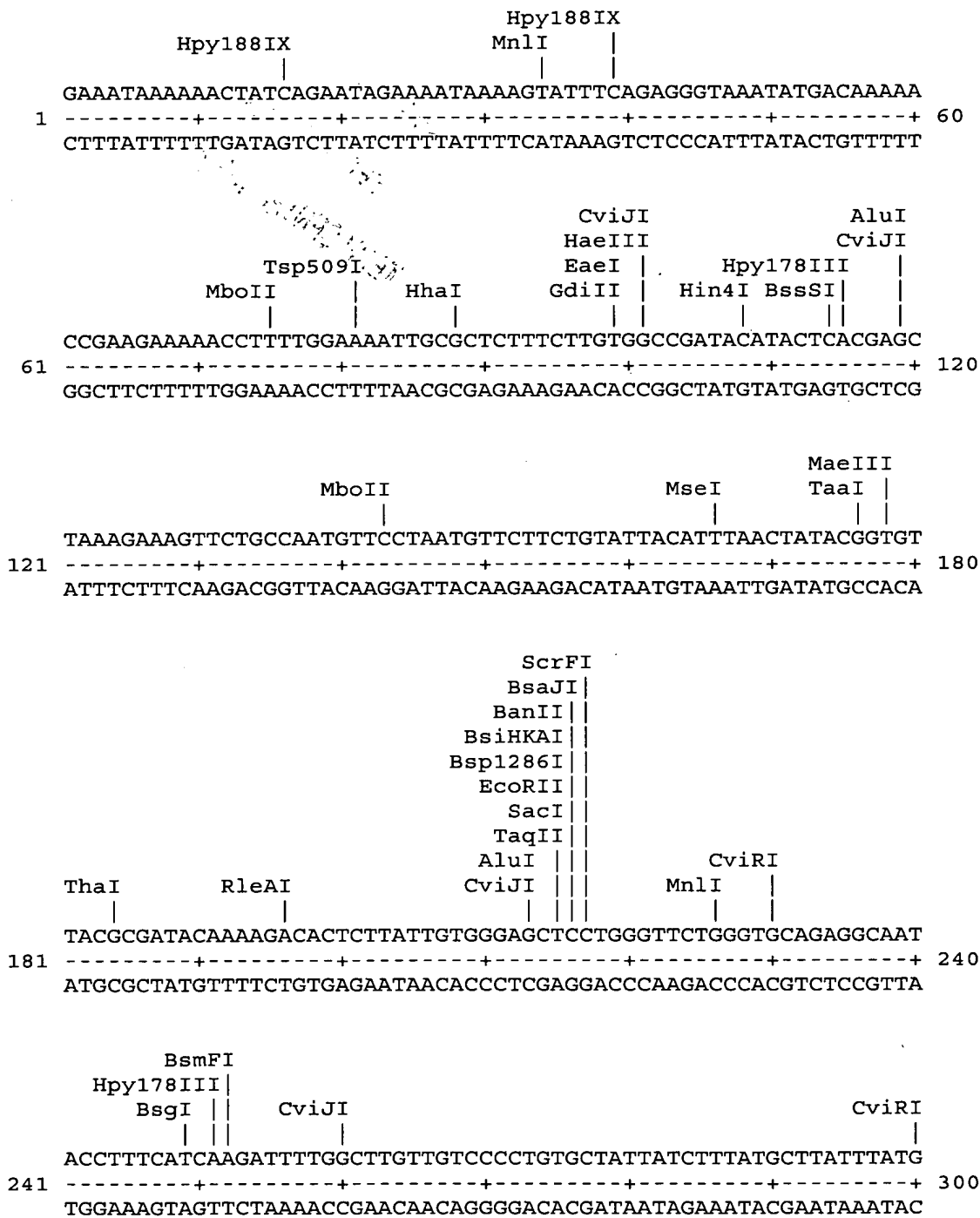
act aaa gaa atg gcc tat atc cct ctt gac caa gag caa aaa gtc aaa	1352
Thr Lys Glu Met Ala Tyr Ile Pro Leu Asp Gln Glu Gln Lys Val Lys	
420 425 430	
ggt aag gct gct att gat gta gtt gcc gcc cgc ttc gga aaa tca gga	1400
Gly Lys Ala Ala Ile Asp Val Val Ala Ala Arg Phe Gly Lys Ser Gly	
435 440 445 450	
gga gct tta atc caa caa ggt ttg ctc gtt atc tgt gga agt att gga	1448
Gly Ala Leu Ile Gln Gln Gly Leu Leu Val Ile Cys Gly Ser Ile Gly	
455 460 465	
gct atg acc cct tat ctt gca gtg att ctt ctt ttc atc att gct att	1496
Ala Met Thr Pro Tyr Leu Ala Val Ile Leu Leu Phe Ile Ile Ala Ile	
470 475 480	
tgg ttg gtt tct gca act aag tta aac aaa cta ttc tta gcg cag tct	1544
Trp Leu Val Ser Ala Thr Lys Leu Asn Lys Leu Phe Leu Ala Gln Ser	
485 490 495	
gct ctt aaa gaa caa gaa gtg gct caa gaa gat tca gct cct gct tct	1592
Ala Leu Lys Glu Gln Glu Val Ala Gln Glu Asp Ser Ala Pro Ala Ser	
500 505 510	
tca tagagttgct tctcttactc ttgttgatcc ctacctgctt tt	1637
Ser	
515	



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Figure 2A: Restriction enzyme analysis of the *C. pneumoniae* ATP/ADP translocase gene.

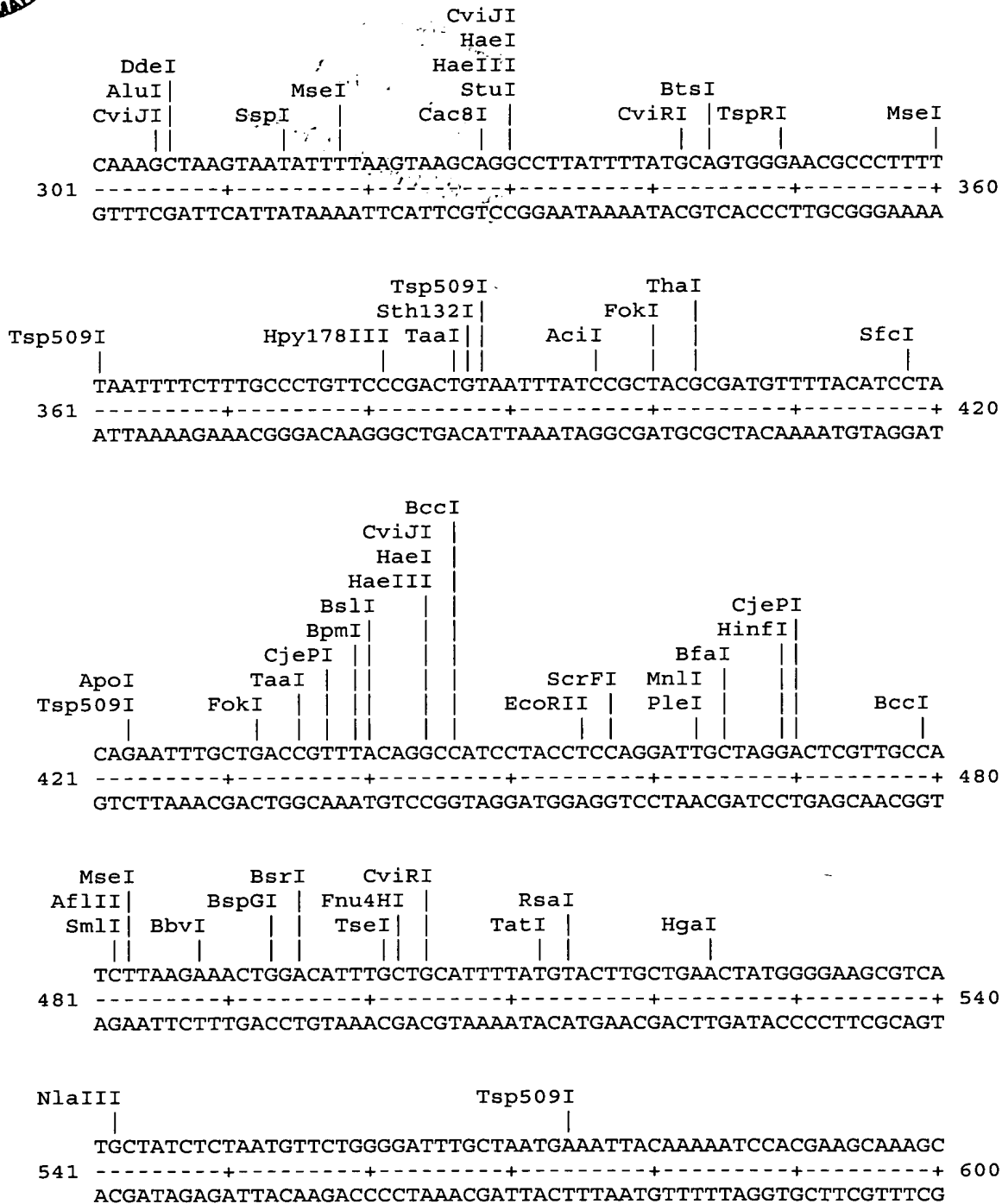




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Figure 2B (Continuation of Figure 2)

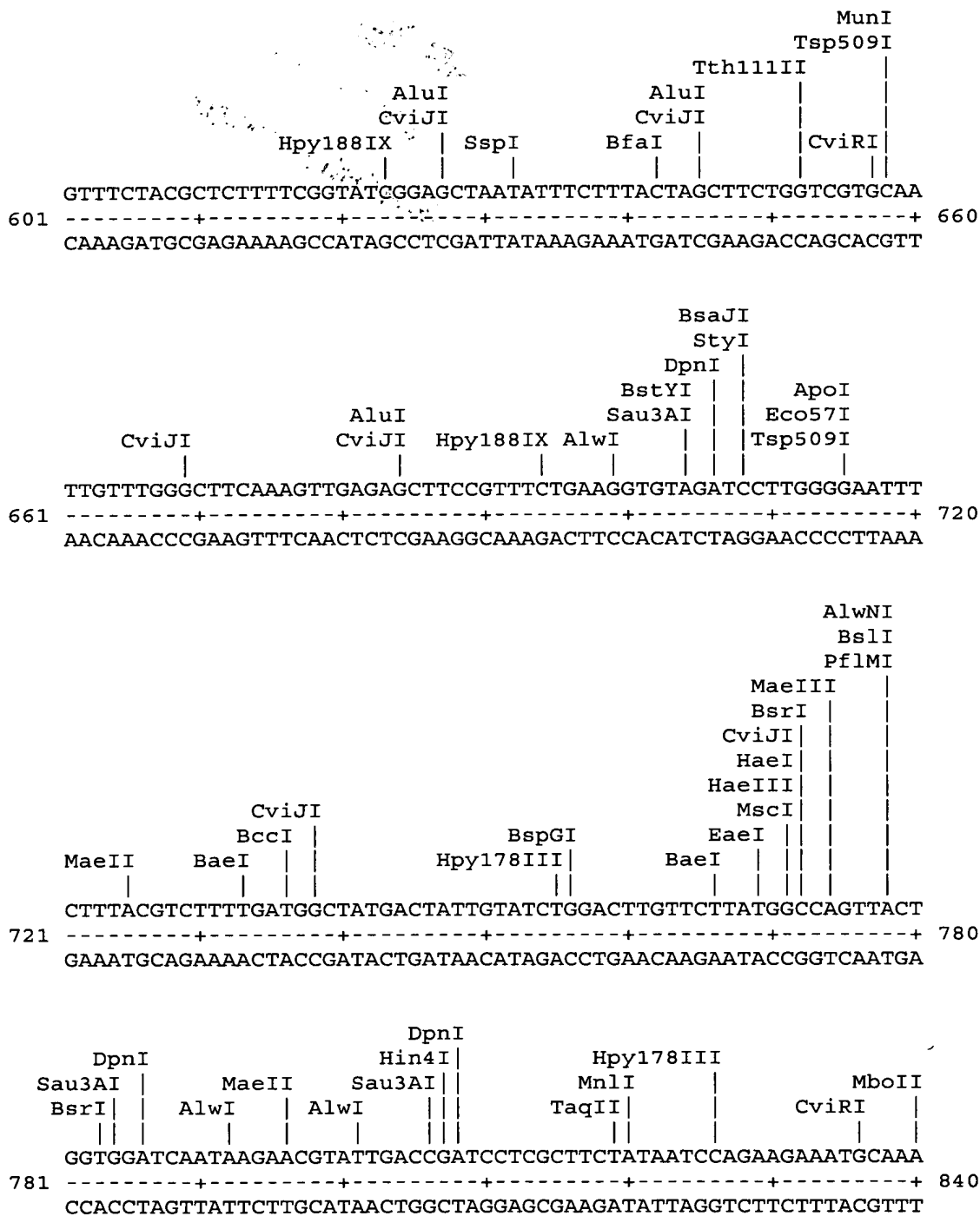




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Figure 2C (Continuation of Figure 2)



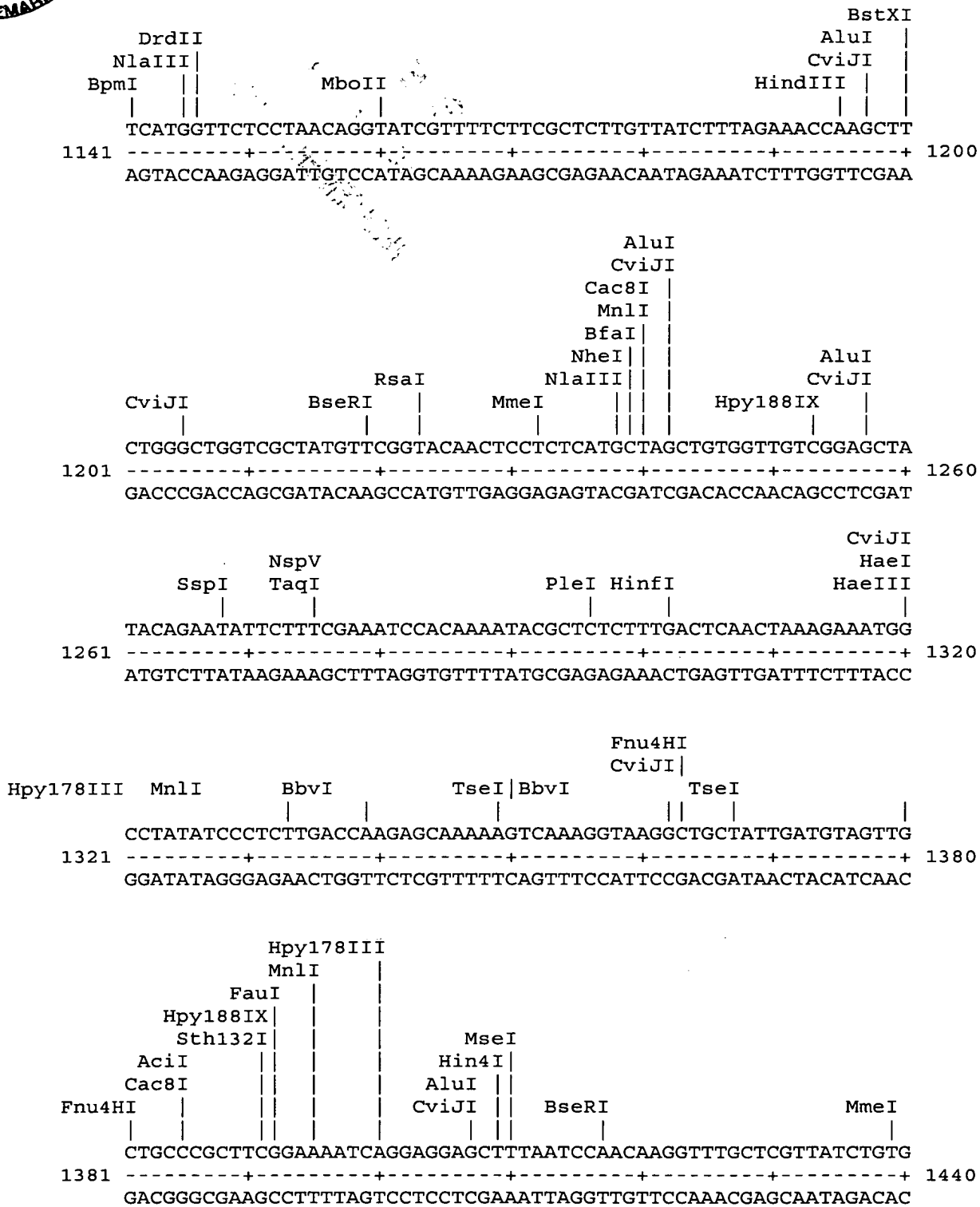




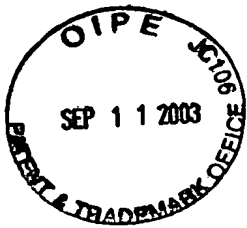
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Figure 2E (Continuation of Figure 2)



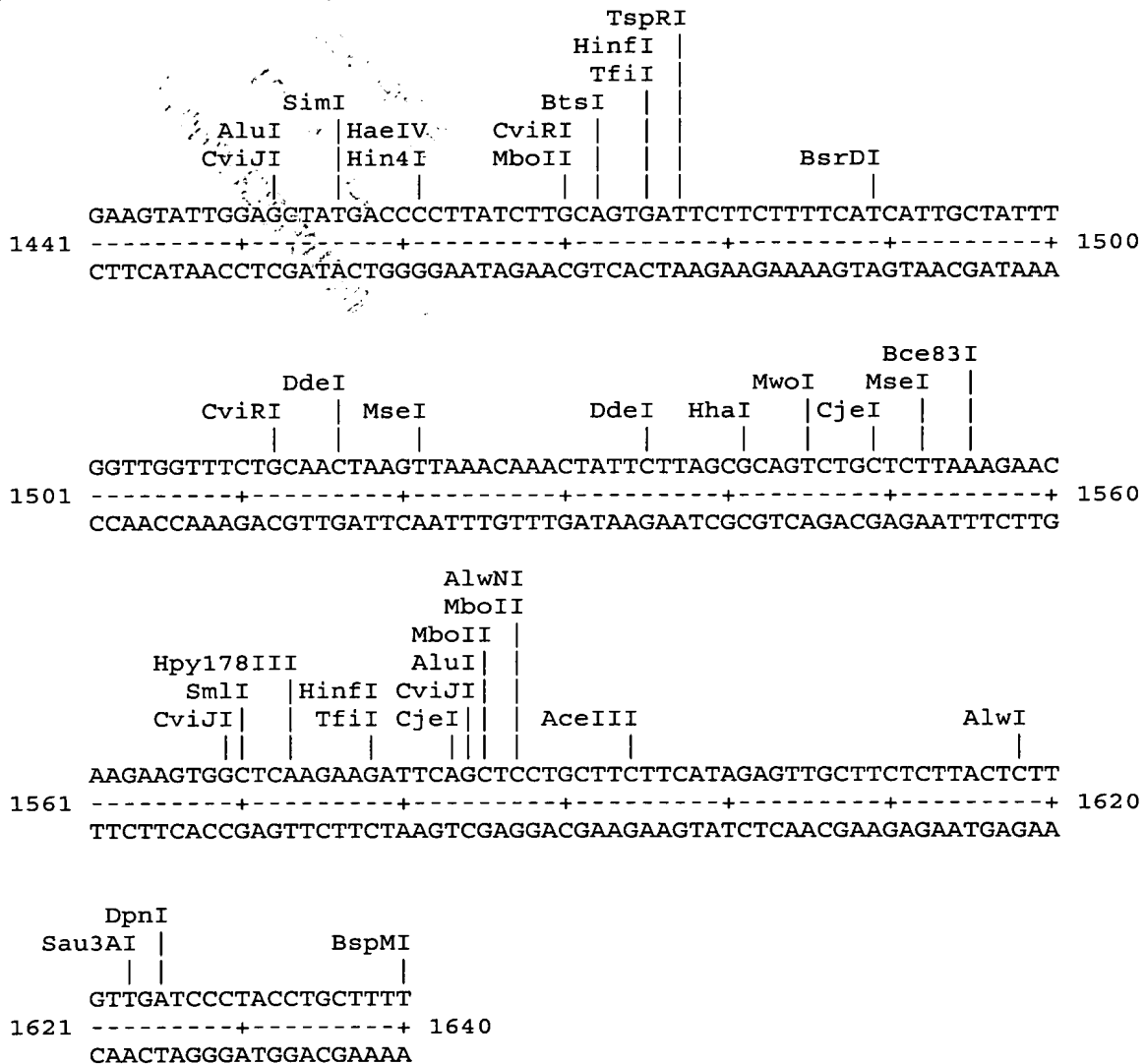




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Figure 2F (Continuation of Figure 2)





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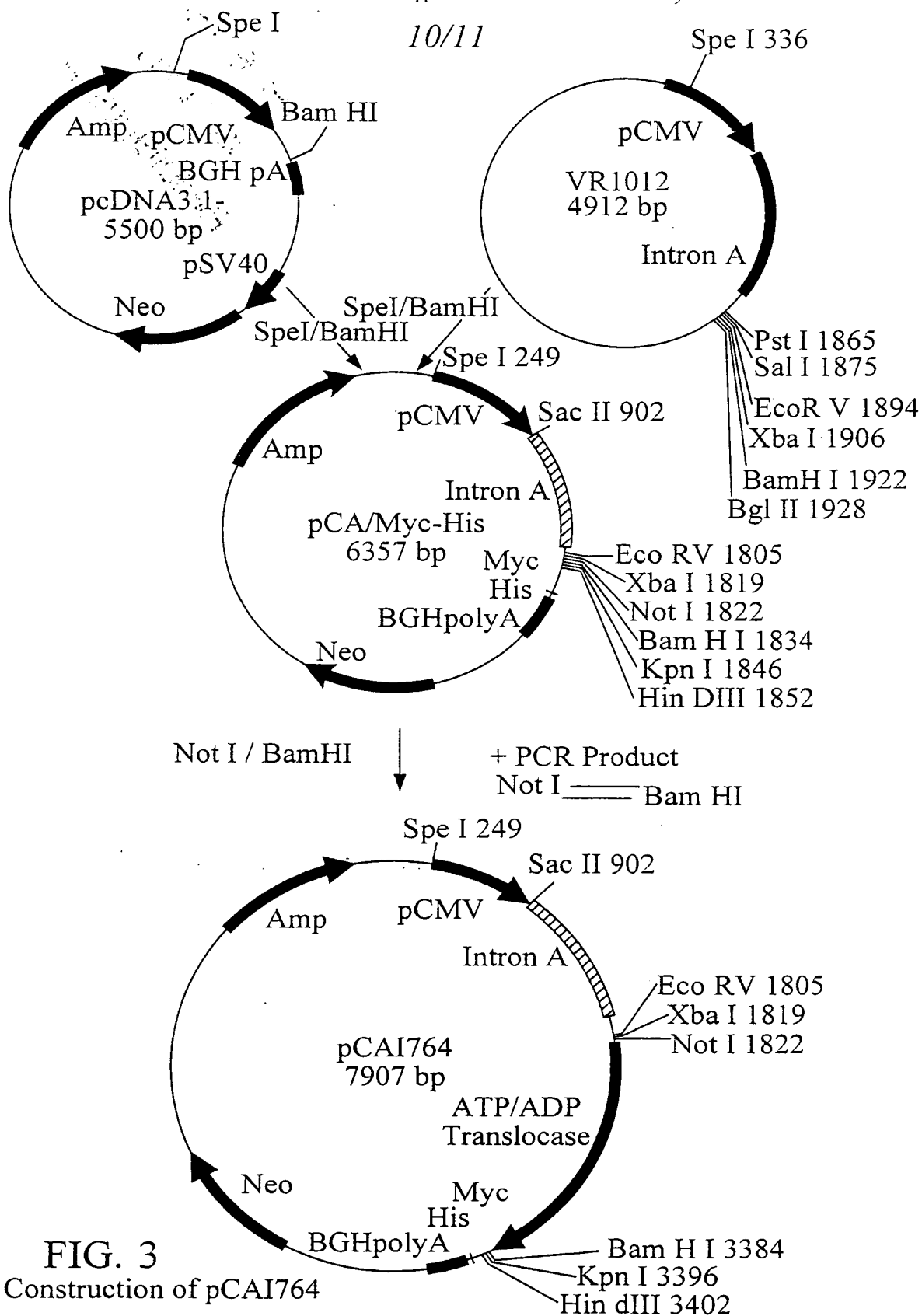


FIG. 3  
Construction of pCAI764



Figure 4: Protective Efficacy of DNA Immunization with pCAI764

